

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/663,618DATE: 08/12/96
TIME: 14:23:54

INPUT SET: S12085.raw

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

Does Not Comply
SEQUENCE LISTING Corrected Diskette Needed

(1) General Information:

(i) APPLICANT: Gray, Patrick W.

(ii) TITLE OF INVENTION: Chitinase Materials and Methods

(iii) NUMBER OF SEQUENCES: 15

*Please review this response.
Many more are shown.*

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
(B) STREET: 6300 Sears Tower, 233 South Wacker Drive
(C) CITY: Chicago
(D) STATE: Illinois
(E) COUNTRY: United States of America
(F) ZIP: 60606-6402

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Rin-Laures, Li-Hsien
(B) REGISTRATION NUMBER: 33,547
(C) REFERENCE/DOCKET NUMBER: 27866/32960

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 312/474-6300
(B) TELEFAX: 312/474-0448
(C) TELEX: 25-3856

*See
attached*

ERRORED SEQUENCES FOLLOW:

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/663,618DATE: 08/12/96
TIME: 14:23:58

INPUT SET: S12085.raw

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1636 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..1399

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 65..1399

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

40 C ATG GTG CGG TCT GTG GCC TGG GCA GGT TTC ATG GTC CTG CTG ATG 46
41 Met Val Arg Ser Val Ala Trp Ala Gly Phe Met Val Leu Leu Met
42 (i) SEQUENCE CHARACTERISTICS:
43 (A) LENGTH: 1636 base pairs last line reads 1645?
44 (B) TYPE: nucleic acid
45 (C) STRANDEDNESS: single
46 (D) TOPOLOGY: linear
47
48 (ii) MOLECULE TYPE: cDNA
49
50 (ix) FEATURE:
51 (A) NAME/KEY: CDS
52 (B) LOCATION: 2..1399
53
54 (ix) FEATURE:
55 (A) NAME/KEY: mat_peptide
56 (B) LOCATION: 65..1399
57
58 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
59
60 C ATG GTG CGG TCT GTG GCC TGG GCA GGT TTC ATG GTC CTG CTG ATG 46
61 Met Val Arg Ser Val Ala Trp Ala Gly Phe Met Val Leu Leu Met
62 -21 -20 -15 -10
63
64 ATC CCA TGG GGC TCT GCT GCA AAA CTG GTC TGC TAC TTC ACC AAC TGG 94
65 Ile Pro Trp Gly Ser Ala Ala Lys Leu Val Cys Tyr Phe Thr Asn Trp
66 -5 1 5 10
67
68 GCC CAG TAC AGA CAG GGG GAG GCT CGC TTC CTG CCC AAG GAC TTG GAC 142
69 Ala Gln Tyr Arg Gln Gly Glu Ala Arg Phe Leu Pro Lys Asp Leu Asp
70 15 20 25
71
72 CCC AGC CTT TGC ACC CAC CTC ATC TAC GCC TTC GCT GGC ATG ACC AAC 190
73 Pro Ser Leu Cys Thr His Leu Ile Tyr Ala Phe Ala Gly Met Thr Asn
74 30 35 40
75
76 CAC CAG CTG AGC ACC ACT GAG TGG AAT GAC GAG ACT CTC TAC CAG GAG 238
77 His Gln Leu Ser Thr Thr Glu Trp Asn Asp Glu Thr Leu Tyr Gln Glu
78 45 50 55
79
80 TTC AAT GGC CTG AAG AAG ATG AAT CCC AAG CTG AAG ACC CTG TTA GCC 286
81 Phe Asn Gly Leu Lys Lys Met Asn Pro Lys Leu Lys Thr Leu Leu Ala
82 60 65 70
83
84 ATC GGA GGC TGG AAT TTC GGC ACT CAG AAG TTC ACA GAT ATG GTA GCC 334
85 Ile Gly GIGTTT CCCTGCTGAA TGCCTCGCTC 900
86
87 CCTTCAAGAC GAGGGGACAGG GAAGGACAGG ACCCTCAGGA ATTCAGTGCC TTCAACAACG 960
88
89 TGAGAGAAAG AGAGAAGCCA GCCACAGACC CCTGGGAGCT TCCGCTTTGA AAGAAGCAAG 1020
90
91 ACACGTGGCC TCGTGAGGGG CAAGCTAGGC CCCAGAGGCC CTGGAGGTCT CCAGGGGCGCT 1080
92

Also see
error
herebig
jump
in
numbers

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/663,618DATE: 08/12/96
TIME: 14:24:04

INPUT SET: S12085.raw

93 GCAGAAGGAA AGAAGGGGGC CCTGCTACCT GTTCTTGGGC CTCAGGCTCT GCACAGACAA 1140
94
95 GCAGCCCTTG CTTTCGGAGC TCCTGTCCAA AGTAGGGATG CGGATCCTGC TGGGGCCGCC 1200
96
97 ACGGCCTGGT GGTGGGAAGG CCGGCAGCGG GCGGAGGGGA TCCAGCCACT TCCCCCTCTT 1260
98
99 CTTCTGAAGA TCAGAACATT CAGCTCTGGA GAACAGTGGT TGCCTGGGGG CTTTTGCCAC 1320
100
101 TCCTTGTCCT CCGTGATCTC CCCTCACACT TTGCCATTTG CTTGTACTGG GACATTGTTC 1380
102
103 TTTCCGGCCG AGGTGCCACC ACCCTGCCCC CACTAAGAGA CACATACAGA GTGGGCCCCG 1440
104
105 GGCTGGAGAA AGAGCTGCCT GGATGAGAAA CAGCTCAGCC AGTGGGGATG AGGTCACCAG 1500
106
107 GGGAGGAGCC TGTGCGTCCC AGCTGAAGGC AGTGGCAGGG GAGCAGGTTC CCCAAGGGCC 1560
108
109 CTGGCACCCC CACAAGCTGT CCCTGCAGGG CCATCTGACT GCCAAGCCAG ATTCTCTTGA 1620
110
111 ATAAAGTATT CTAGTGTGGA AACGC 1645
112

257 (2) INFORMATION FOR SEQ ID NO:8:
258259 (i) SEQUENCE CHARACTERISTICS:
--> 260 (A) LENGTH: 170 base pairs

261 (B) TYPE: nucleic acid

262 (C) STRANDEDNESS: single

263 (D) TOPOLOGY: unknown
264
265
266267 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
268269 Met Pro Val Met Arg Leu Phe Pro Cys Phe Leu Gln Leu Leu Ala Gly
270 1 5 10 15271
272 Leu Ala Leu Pro Ala Val Pro Pro Gln Gln Trp Ala Leu Ser Ala Gly
273 20 25 30274
275 Asn Gly Ser Ser Glu Val Glu Val Val Pro Phe Gln Glu Val Trp Gly
276 35 40 45277
278 Arg Ser Tyr Cys Arg Ala Leu Glu Arg Leu Val Asp Val Val Ser Glu
279 50 55 60280
281 Tyr Pro Ser Glu Val Glu His Met Phe Ser Pro Ser Cys Val Ser Leu
282 65 70 75 80283
284 Leu Arg Cys Thr Gly Cys Cys Gly Asp Glu Asn Leu His Cys Val Pro
285 85 90 95286
287 Val Glu Thr Ala Asn Val Thr Met Gln Leu Leu Lys Ile Arg Ser Gly
288 100 105 110

only 169 shown.

See more detail
in attached paper

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/663,618DATE: 08/12/96
TIME: 14:24:09

INPUT SET: S12085.raw

289
290 Asp Arg Pro Ser Tyr Val Glu Leu Thr Phe Ser Gln His Val Arg Cys
291 115 120 125
292
293 Glu Cys Arg Pro Leu Arg Glu Lys Met Lys Pro Glu Arg Arg Arg Pro
294 130 135 140
295
296 Lys Gly Arg Gly Lys Arg Arg Arg Glu Lys Gln Arg Pro Thr Asp Cys
297 145 150 155
298
299 His Leu Cys Gly Asp Ala Val Pro Arg Arg ← 169
300 160 165
301 (i) SEQUENCE CHARACTERISTICS:
302 (A) LENGTH: 12 amino acids
303 (B) TYPE: amino acid
304 (C) STRANDEDNESS: single
305 (D) TOPOLOGY: linear
306
307 (ii) MOLECULE TYPE: peptide
308
--> 309 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:
310
311 Trp Arg Lys Phe Ala Leu Leu Gly Ser Gly Pro Thr
312 1 5 10
313
314

--> 315 (2) INFORMATION FOR SEQ ID NO:159:
316
317 (i) SEQUENCE CHARACTERISTICS:
318 (A) LENGTH: 12 amino acids
319 (B) TYPE: amino acid
320 (C) STRANDEDNESS: single
321 (D) TOPOLOGY: linear
322
323 (ii) MOLECULE TYPE: peptide
324
325 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:
326
327 His Arg Ala Tyr Arg Ile Ala Thr Met Phe Ser Gly
328 1 5 10
329
330

*See
next
page*

363 (2) INFORMATION FOR SEQ ID NO:162:
364
365 (i) SEQUENCE CHARACTERISTICS:
366 (A) LENGTH: 12 amino acids
367 (B) TYPE: amino acid
368 (C) STRANDEDNESS: single
369 (D) TOPOLOGY: linear
370
371 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Pro	Val	Met	Arg	Leu	Phe	Pro	Cys	Phe	Leu	Gln	Leu	Leu	Ala	Gly	
1				5					10					15		
Leu	Ala	Leu	Pro	Ala	Val	Pro	Pro	Gln	Gln	Trp	Ala	Leu	Ser	Ala	Gly	
			20					25					30			
Asn	Gly	Ser	Ser	Glu	Val	Glu	Val	Val	Pro	Phe	Gln	Glu	Val	Trp	Gly	
		35					40					45				
Arg	Ser	Tyr	Cys	Arg	Ala	Leu	Glu	Arg	Leu	Val	Asp	Val	Val	Ser	Glu	
	50					55					60					
Tyr	Pro	Ser	Glu	Val	Glu	His	Met	Phe	Ser	Pro	Ser	Cys	Val	Ser	Leu	
65					70					75					80	
Leu	Arg	Cys	Thr	Gly	Cys	Cys	Gly	Asp	Glu	Asn	Leu	His	Cys	Val	Pro	
				85					90					95		
Val	Glu	Thr	Ala	Asn	Val	Thr	Met	Gln	Leu	Leu	Lys	Ile	Arg	Ser	Gly	
			100					105					110			
Asp	Arg	Pro	Ser	Tyr	Val	Glu	Leu	Thr	Phe	Ser	Gln	His	Val	Arg	Cys	
		115					120					125				
Glu	Cys	Arg	Pro	Leu	Arg	Glu	Lys	Met	Lys	Pro	Glu	Arg	Arg	Arg	Pro	
	130					135					140					
Lys	Gly	Arg	Gly	Lys	Arg	Arg	Arg	Glu	Lys	Gln	Arg	Pro	Thr	Asp	Cys	
	145					150					155					
His	Leu	Cys	Gly	Asp	Ala	Val	Pro	Arg	Arg							
160						165										

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

*main heading missing.
Also, this jumps from
Seq. 8 to 158?*

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Trp	Arg	Lys	Phe	Ala	Leu	Leu	Gly	Ser	Gly	Pro	Thr
1				5					10		

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

His Arg Ala Tyr Arg Ile Ala Thr Met Phe Ser Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Arg Gly Leu Met Arg Arg Ser Thr Lys Thr Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Ala Arg His Arg Met Phe Gln Trp Ala Met Val Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Ile	Met	Ile	Gly	Lys	Glu	Gly	Ala	Val	Ser	Ser	Ser
1				5					10		

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
 (B) CLONE: 73 2 0.5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Trp Gln Asn Arg Thr His Lys Val Val Ser Gly Arg
1 5 10

Now it
is back to
seq. 24.77
I continues
on to
seq. 70.

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
 (B) CLONE: 78 2 1.1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ala Arg Lys His Lys Val Thr
1 5

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
 (B) CLONE: 40 3 1.1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Arg Gln Val Thr Arg Leu His Lys Val Ile His
1 5 10